

## CLUSTAL W (1.82) multiple sequence alignment

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gi|74716|pir|VCLJSA -----
gi|9627213|ref|NP_056894.1| -----
gi|1706658|sp|P51515|ENV_SRV2 -----
gi|119398|sp|P10269|ENV_BAEVM -----
gi|1143545|emb|CAA61093.1| -----
gi|9627018|ref|NP_041262.1| -----
gi|11055586|gb|AAG28161.1|AF28 -----
gi|28927670|gb|AAF81698.2|AF24 -----
gi|20149612|ref|NP_055405.2| -----
gi|13310191|gb|AAK18189.1|AF33 -----
gi|8439396|emb|CAB94192.1| -----
gi|16024911|gb|AAL11491.1| -----
gi|27734142|ref|NP_775596.1| -----
gi|119466|sp|P23064|ENV_HTL1M -----
gi|119467|sp|P03383|ENV_HTLV2 -----
gi|4027915|gb|AAC96087.1| -----
gi|74689|pir|VCLJGL -----MVLL
gi|74707|pir|VCMVSS -----
gi|119431|sp|P04582|ENV_HV1B8 -----
gi|74661|pir|VCLJSI -----
gi|119462|sp|P04577|ENV_HV2RO -----
gi|74682|pir|VCLJVS MASKEKPSRRTTWRDMEPPLRETWNQVLQELVKRQQQEEEEQQGLVSG
gi|74722|pir|VCLJLK -----MAPPMMNLQQWLLWKKMNETHLALENISLSTEEQKQQVIEIQ
gi|12958609|gb|AAK09373.1|AF32 -----
gi|6016596|sp|O61703|MPCP_CHOF -----

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gi|74716|pir|VCLJSA -----MNFNHH
gi|9627213|ref|NP_056894.1| -----MNFNYH
gi|1706658|sp|P51515|ENV_SRV2 -----MTLKDI
gi|119398|sp|P10269|ENV_BAEVM -----MGFTT-
gi|1143545|emb|CAA61093.1| -----MKLPT-
gi|9627018|ref|NP_041262.1| -----MLCILILLLHP-
gi|11055586|gb|AAG28161.1|AF28 -----MISTLLISL-
gi|28927670|gb|AAF81698.2|AF24 -----MDCLTNLRS AEG
gi|20149612|ref|NP_055405.2| -----
gi|13310191|gb|AAK18189.1|AF33 -----
gi|8439396|emb|CAB94192.1| -----MIFAGKAPSNTSTLMKFY
gi|16024911|gb|AAL11491.1| -----MIFAGKAPSNTSTLMKFY
gi|27734142|ref|NP_775596.1| -----
gi|119466|sp|P23064|ENV_HTL1M -----MGKFLATLIL
gi|119467|sp|P03383|ENV_HTLV2 -----MGNVFFLLLF
gi|4027915|gb|AAC96087.1| -MLLTSSLHHPRHQMSPGSKRLIIL-LSCVFGGGGTSLQNKPNHQPM
gi|74689|pir|VCLJGL SMLLTSSLHHLRHQMSPGSKRLIIL-LSCVFGGGGTSLQNKPNHQPM
gi|74707|pir|VCMVSS ---MEGPTHPKPFKDKTF SWDLIILVGVVRVLLRLDVGMANPSPHQVY
gi|119431|sp|P04582|ENV_HV1B8 -----MRVKEKYQHLWRWGWRGTMLLGLMICSAT-EKLWVTV
gi|74661|pir|VCLJSI -----MKVMEKKKRWDNS-LSIITIITIIILLTPCLT-SELWVTV
gi|119462|sp|P04577|ENV_HV2RO -----MMNQLLIAILLASACL VYCTQYVTV
gi|74682|pir|VCLJVS KSWVSIDLLGTEGKDIKKVNIWEPCEKWFQAQVWVGLVWLQIVLWGL
gi|74722|pir|VCLJLK EVIPTRM DRV KYL AY ACCATSTRVMCWLFLICVLLIIVFVSCFVTVAR
gi|12958609|gb|AAK09373.1|AF32 -----MDQWLLWFGYLVASTYGLSLRHRHQ SVGTPTAE
gi|6016596|sp|O61703|MPCP_CHOF -----

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gi|74716|pir|VCLJSA WSLVVISQIFQVQAGFGDPREALLEIQQKHGKPCDCAGGYVSS-----
gi|9627213|ref|NP_056894.1| WSLVILSQISQVQAGFGDPREALAEIQQKHGKPCDCAGGYVSS-----
gi|1706658|sp|P51515|ENV_SRV2 WRVLLIFQTARVYAGFGDPREAITMIHQHKGKPCDCAGGYVNA-----

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gi | 119398 | sp | P10269 | ENV_BAEVM      -KIIFLYNLVLVYAGFDDPRKAIELVQKRYGRPCDCSGGQVSE-----
gi | 1143545 | emb | CAA61093.1 |          -GMVILCSLIIVRAGFDDPRKAIALVQKQHGKPCCECSGGQVSE-----
gi | 9627018 | ref | NP_041262.1 |          -----RLCPVTKGGLG-KPSG-DIYTALFGAPCDCKGGTQTNN---Y
gi | 11055586 | gb | AAG28161.1 | AF28      -----LLFAETDAGFG-PPPGTDLRHALFGAPCDCKGGIIT-----A
gi | 28927670 | gb | AAF81698.2 | AF24      DQAGKTLILLVWVWGF- TTAEGYPLQQLWGLPCDCSGGYVFS-----
gi | 20149612 | ref | NP_055405.2 |          -----MALPYHIFLFTVLLPSFTLTAPPPRCMT-----
gi | 13310191 | gb | AAK18189.1 | AF33      -----MALPYHTFLFTVLLPPFALTAPPPCCCTT-----
gi | 8439396 | emb | CAB94192.1 |          LLYSLLFSFPFLCHPLPLPSYLHHTINLTHSLLAASNPSLVNNC---W
gi | 16024911 | gb | AAL11491.1 |          LLYSLLFSFPFLCHPLPLPSYLHHTINLTHSLLAASNPSLVNNC---W
gi | 27734142 | ref | NP_775596.1 |          MTGFWVLCFVLPSSLSYPESWMPVLVNLTHHILRDTNSSLSFSNC---W
gi | 119466 | sp | P23064 | ENV_HTL1M    QFCPLILGDYSPSCCTLTIG-----VSSYHSKPCNPAQPVCSSWT---L
gi | 119467 | sp | P03383 | ENV_HTLV2    THFPLAQ----QSRCTLTIG-----ISSYHSSPCSPTQPVCTWN---L
gi | 4027915 | gb | AAC96087.1 |          TWQVLS-QTGDVVWVTEAVQPLWTWVPSLKPDCVICALAAGLESWD---I
gi | 74689 | pir | | VCLJGL      TWQVLS-QTGDVVWDTKAVQPPWTWVPTLKPDCVICALAASLESWD---I
gi | 74707 | pir | | VCMVSS      TWVITNVQTNQANATSMGLTLDAYPTLHVLDLCLVGG--DTWE---P
gi | 119431 | sp | P04582 | ENV_HV1B8    GVPVWKEATTTLFCASDAKAYDTEVHNVWATHACVPTDPNPQEV---V
gi | 74661 | pir | | VCLJSI      GVPVWHDADPVLFCASDAKAHSTEAHNIWATQACVPTDPSPEV---F
gi | 119462 | sp | P04577 | ENV_HV2RO    GVPTWKNATIPLFCA-----TRNRDTWGTIQCLPDNDYQEI---T
gi | 74682 | pir | | VCLJVS      EVRKGNGQCQAEVIEDLVSDPGGFQRVQHVETVPVTCVTKNFTQWGCQP
gi | 74722 | pir | | VCLJLK      WNRDINVFGPVIDWNVTHQATYQQLKAARLTRSLKVEHPHISYIS- IN
gi | 12958609 | gb | AAK09373.1 | AF32      EPQILIEDTDHVFRQRASDMFAQEPEYTEKRNLRNHRREFSGNQDTD
gi | 6016596 | sp | O61703 | MPCP_CHOF    -----MFSLLLEAAKSSPFHGPLTPARCDAPAQGMAAS-----

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gi | 74716 | pir | | VCLJSA      TNSLTTVSCSTYTAYSVTNS-----LKWQCVSTPT-----
gi | 9627213 | ref | NP_056894.1 |          INSLTTVSCSTHTAYSVTNS-----LKWQCVSTPT-----
gi | 1706658 | sp | P51515 | ENV_SRV2      TVYLAAVSCSSHTAYQPSDS-----LKWRCVSNPT-----
gi | 119398 | sp | P10269 | ENV_BAEVM      SDRVSQVTCSGKTAYLMPD-----QRWKCKSIPK-----
gi | 1143545 | emb | CAA61093.1 |          PNSIQQVTCPGKTAYLMTN-----QKWKCRVTPK-----
gi | 9627018 | ref | NP_041262.1 |          PITYTQVTDGDKNAYLTYDT-----NWNGVSSPKWLCVRKPPS-----
gi | 11055586 | gb | AAG28161.1 | AF28      TAFTRAIDCGNKIAYLQYHH-----TGTGISRQSYQCVRKVKI-----
gi | 28927670 | gb | AAF81698.2 | AF24      TYYTNSLDCGSSTAYLTYGSGTGSWGWGGGFRQWECVFKPKI-----
gi | 20149612 | ref | NP_055405.2 |          SPYQEFLLWRMQRPGNIDAPS-----YRSLSKGT-----
gi | 13310191 | gb | AAK18189.1 | AF33      SPYQEFLLWRTRLPGNIDAPS-----YRSLSKGN-----
gi | 8439396 | emb | CAB94192.1 |          ISLSSSAYTAVPAVQTDWATSP-----ISLHLRTSFN-----
gi | 16024911 | gb | AAL11491.1 |          ISLSSSAYTAVPTLQTDWATSP-----ISLHLRTSCN-----
gi | 27734142 | ref | NP_775596.1 |          LSTQTQRSLAVPAPLSIWTDTPT-----MKLHLTYSVRPFSGSF
gi | 119466 | sp | P23064 | ENV_HTL1M    LALSADQALQPPCPNLVSY-----SSYHATYSLY-----
gi | 119467 | sp | P03383 | ENV_HTLV2    NSLTTDQRLHPPCPNLITY-----SGFHKTYSLY-----
gi | 4027915 | gb | AAC96087.1 |          SDVSASKRIRPLDSNYNNANKQ--ISWGAIGCSYPRARTRIA-----
gi | 74689 | pir | | VCLJGL      TDVSSSKRVRPPDSDYTAAYKQ--ITWGAIGCSYPRARTRMA-----
gi | 74707 | pir | | VCMVSS      LDPSNVKHG---ARYSSS-----KYGCKTTDRKKQQQ-----
gi | 119431 | sp | P04582 | ENV_HV1B8    NVTENFNMMWKNMVEQMHEDIIS-----LWDQSLKPCVKLTPL
gi | 74661 | pir | | VCLJSI      NVIESFNMMWKNMVDQMHEDIIS-----LWDQSLKPCVKLTPL
gi | 119462 | sp | P04577 | ENV_HV2RO    -VTEAFDAWNNTVTEQAIEDVWH-----LFETS IKPCVKLTPL
gi | 74682 | pir | | VCLJVS      AYPDPELEYRNI SREILEEVYKQDWPWNTYHWPWQWENMRQWMEKENE
gi | 74722 | pir | | VCLJLK      SIPQGVMYTPHPEPIILKERV LGISQVLMINSENIANVANLSQETKVL
gi | 12958609 | gb | AAK09373.1 | AF32      SSGETY SAYTSDDPLI IHTNKG-----KIRGITQTATTG---
gi | 6016596 | sp | O61703 | MPCP_CHOF    -----

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gi | 74716 | pir | | VCLJSA      TASPT-HIGSCPSQCNSQSYDSVHA-----
gi | 9627213 | ref | NP_056894.1 |          TPSNT-HIGSCPGECONTISYDSVHA-----
gi | 1706658 | sp | P51515 | ENV_SRV2      LANGE-NIGNCP--CKTFK-ESVHS-----
gi | 119398 | sp | P10269 | ENV_BAEVM      DTSPSGLQECPC--CNSYQ-BSVHS-----
gi | 1143545 | emb | CAA61093.1 |          ISPSGGELQNCPC--CNTFQ-DSMHS-----
gi | 9627018 | ref | NP_041262.1 |          IPVINGRPGPCPSECTNNIKSQMHS-----
gi | 11055586 | gb | AAG28161.1 | AF28      IPQNNIGIPGPCSDCVY--LQALHS-----
gi | 28927670 | gb | AAF81698.2 | AF24      IPSVQGPQGPCPSECLT-IATQMHS-----
gi | 20149612 | ref | NP_055405.2 |          -----PTFTAHTHMPR-----

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gi | 13310191 | gb | AAK18189.1 | AF33 -----STFTAHTHMPR-----
gi | 8439396 | emb | CAB94192.1 | -----SPHLYPPEELIYFLDRSSKT-----
gi | 16024911 | gb | AAL11491.1 | -----SPHLYPPEELIYFLDRSSKT-----
gi | 27734142 | ref | NP_775596.1 | SDIERRRLRFRPLTASYSFHNPD RR-----
gi | 119466 | sp | P23064 | ENV_HTL1M LFPHWIKKPNRNGGGYYSASYS DPC-----
gi | 119467 | sp | P03383 | ENV_HTLV2 LFPHWIKKPNRQGLGYYS P SYNDPC-----
gi | 4027915 | gb | AAC96087.1 | NSPFYVCPRDGRTLS -EARRCGELE-----
gi | 74689 | pir | | VCLJGL SSTFYVCPRDGRTLS -EARRCGGLE-----
gi | 74707 | pir | | VCMVSS TYPFYVCPGHAPSMGPKGTHCGGAH-----
gi | 119431 | sp | P04582 | ENV_HV1B8 SLKCTDLKNDTNTNSSSGRMIMEKG-----
gi | 74661 | pir | | VCLJSI TLQCSKANFSQAKNLTN -QTSSPPL-----
gi | 119462 | sp | P04577 | ENV_HV2RO AMKCSSTESSTGNNTTSKSTSTTTTTPTDQEQEISEDTPCARADNCSG
gi | 74682 | pir | | VCLJVS YKERTNKTKEDIDDLVAGRIRGRFCVPYPYALLRCEEWCWPESINQF
gi | 74722 | pir | | VCLJLK DMINEELQDLSNQMIDFELPLGDPR-----D
gi | 12958609 | gb | AAK09373.1 | AF32 KLVDAWLGIPIYAKKPIGDLRFRHPR-----
gi | 6016596 | sp | O61703 | MPCP_CHOF -----

gi | 74716 | pir | | VCLJSA -----TCYNHYQOCTIGNKTYLTATMIRDKSPSSGDG-----NV
gi | 9627213 | ref | NP_056894.1 | -----SCYNHYQOCNIGNKTYLTATITGDRTPAIGDG-----NV
gi | 1706658 | sp | P51515 | ENV_SRV2 -----SCYTAYQECFFGNKTYTATILASNRAPTIGTS-----NV
gi | 119398 | sp | P10269 | ENV_BAEVM -----SCYTSYQOCSRGNKTYTATLLKTQT---GGT-----SD
gi | 1143545 | emb | CAA61093.1 | -----SCYTEYRQCRRINKTYTATLLKIRS---GSL-----NE
gi | 9627018 | ref | NP_041262.1 | -----SCYSSFSQOCTQGNNTYFTAILQRTKSTSET-----NP
gi | 11055586 | gb | AAG28161.1 | AF28 -----LCYTSTQOCTGKSGTYLTSRQQRAYGGSTGGDW-----GP
gi | 28927670 | gb | AAF81698.2 | AF24 -----TCYEKAQECTLLGKTYFTAILQKTKLGSYE-----
gi | 20149612 | ref | NP_055405.2 | -----NCYHSATLCMHANTHYWTG-----
gi | 13310191 | gb | AAK18189.1 | AF33 -----NCYNSATLCMHANTHYWTG-----
gi | 8439396 | emb | CAB94192.1 | -----SPDISHQAAALLRRTYLKNLSPYIN-----S
gi | 16024911 | gb | AAL11491.1 | -----SPDISHQAAALLRRTYLKNLSPYIN-----S
gi | 27734142 | ref | NP_775596.1 | -----AIAFLQLVSSSTGIFRIITRITSVIYPHKDRFFE-----SA
gi | 119466 | sp | P23064 | ENV_HTL1M -----SLKCPYLGCQSWTTPYTAVSS-----
gi | 119467 | sp | P03383 | ENV_HTLV2 -----SLQCPYLGCQAWTSAYTGPVSS-----
gi | 4027915 | gb | AAC96087.1 | -----SLYCKEWGCETTGNVHWQPRSSWDLITVKWGRNRQWEQNMLS V
gi | 74689 | pir | | VCLJGL -----SLYCKEWDCETTGTGYWLSKSSKDLITVKWDQNSEWTQ-KFQQ
gi | 74707 | pir | | VCMVSS -----DGFCAAWGCETTGEAWWKPTSSWDYITVKRGSS-----QDTS
gi | 119431 | sp | P04582 | ENV_HV1B8 --EIKNCSFNISTSKRGKVQKEYAFFYKLDIIPIDNDTT-----SY
gi | 74661 | pir | | VCLJSI --EMKNCSFNVTTEL RDKKKQVYSLFYVEDVVNLGNENN-----TY
gi | 119462 | sp | P04577 | ENV_HV2RO EEETINCQFNMTGLERDKKKQYNETWYSKDVVCETNNSTN----QTQC
gi | 74682 | pir | | VCLJVS HAEEKIKINCTKAKAVSCTEKMPLAAVQRVYWEKEDEESMKFLNIKACN
gi | 74722 | pir | | VCLJLK QYIHHKCYQEF AHCYLVKYYKPKSPWISEGIIVDQCPLPRIHDP-NYYK
gi | 12958609 | gb | AAK09373.1 | AF32 ---PIDRWDTTTTPETILNCTTPPNTCVQIFDITLFGDFPG-----A
gi | 6016596 | sp | O61703 | MPCP_CHOF -----AAPVGDSCFEFGSTKYFALCG-----

gi | 74716 | pir | | VCLJSA IILGNNQNLI IAGCPENKKGQVVCWNSQPSVHMSDG-----GG
gi | 9627213 | ref | NP_056894.1 | VLGTSHNLIITAGCPNGKKGQVVCWNSRPSVHISDG-----GG
gi | 1706658 | sp | P51515 | ENV_SRV2 VLGNTHNLLSAGCTGN-VGQPICWNPKAPVHISDG-----GG
gi | 119398 | sp | P10269 | ENV_BAEVM VLGSTNKLIQSPCNGI-KGQSI CWSTTAPIHVS DG-----GG
gi | 1143545 | emb | CAA61093.1 | ILQNP NQLLQSPCRGS-INQPVCWSATAPIHISDG-----GG
gi | 9627018 | ref | NP_041262.1 | SGLQPHGVLQAGCDGT-VGKSVCWNQQAPIHVS DG-----GG
gi | 11055586 | gb | AAG28161.1 | AF28 ISGPTNKY AQASCDKINIGKNVCWSLHAPIHVS DG-----GG
gi | 28927670 | gb | AAF81698.2 | AF24 --DGPNKLLQASCTGT-IGKPV CWDPVAPVYVSDG-----GG
gi | 20149612 | ref | NP_055405.2 | -----KMINPSCP GG-LGVTVCWTYFTQTGMSDG-----GG
gi | 13310191 | gb | AAK18189.1 | AF33 -----KMINPSCP GG-LGATVCWTYFTHTSMSDG-----GG
gi | 8439396 | emb | CAB94192.1 | PIFGPLTTQTTIPVAAPLCIS---WQRPTGIPLGN-----LS
gi | 16024911 | gb | AAL11491.1 | PIFGPLTTQTTIPVAAPLCIS---WQRPTGIPLGN-----LS
gi | 27734142 | ref | NP_775596.1 | PLWGPLFTETVLR SQAPLCISRFKVSAYATFVGN-----LS
gi | 119466 | sp | P23064 | ENV_HTL1M -PYWKFQQDVNFTQEVS R-----LNINLHFSKC-----GF
gi | 119467 | sp | P03383 | ENV_HTLV2 -PSWKFHSDVNFTQEVS Q-----VSLRLHFSKC-----GS

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gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO  
 gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHOF

QTGWCNPLKIDFTEKGKHSRDWIKGRTWGLRFNVA-----GH  
 QTGWCNPLKIDFTDKGKLSKDWITGKTWGLRFYVS-----GH  
 KN--CNPLVLQFTQKGRQ--ASWDGPKLWGLRLYRT-----GY  
 TSCNTSVITQACPKVSFEPPIPIHYCAPAGFAILKC-----NN  
 INCNTTAITQACPKTSFEPPIPIHYCAPAGFAILKC-----ND  
 NHCNTSVITESCDKHYWDAIRFRYCAPPGYALLRC-----ND  
 LRCQDEGKSPGGCVQGYPIPKGAEI IPEAMKYLRGKKSRYGGIKDKNG  
 PIWDYYLKIQNIRPQGWTSKSYYGRTARMGSFYIPT-----FLR  
 WNPNSPVSEDCLYINVVVVKPRPQNAAMVWVIFGG-----GFY  
 -----LGGILSCGITHTAVVPLDLVKCR-----

gi | 74716 | pir | | VCLJSA  
 gi | 9627213 | ref | NP\_056894.1 |  
 gi | 1706658 | sp | P51515 | ENV\_SRV2  
 gi | 119398 | sp | P10269 | ENV\_BAEVM  
 gi | 1143545 | emb | CAA61093.1 |  
 gi | 9627018 | ref | NP\_041262.1 |  
 gi | 11055586 | gb | AAG28161.1 | AF28  
 gi | 28927670 | gb | AAF81698.2 | AF24  
 gi | 20149612 | ref | NP\_055405.2 |  
 gi | 13310191 | gb | AAK18189.1 | AF33  
 gi | 8439396 | emb | CAB94192.1 |  
 gi | 16024911 | gb | AAL11491.1 |  
 gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO  
 gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHOF

DKVREIIVNKKFEELHKSLSFPELSYHPLAL-----PEARGKEK  
 DKARDIIVNKKFEELHRSLSFPELSYHPLAL-----PEARGKEK  
 DKAREIAVQKRLEEIHKSLSFPELRYHPLAL-----PKARGKEK  
 DTTRIKSVQRKLEEIHKALYPELQYHPLAI-----PKVRDNL  
 DTKRVVTVQKRLEQIHKAMTPELQYHPLAL-----PKVRDDL  
 DAVRELYVQKQIELVIQSQFPKLSYHPLAR-----SKPRG-PD  
 DQIREMEVKERVDEIIRAMYPPLOQYHPLAL-----PRGRG-VD  
 DMIREESVREERLEEIRHSYPSVQYHPLAL-----PRPRG-VD  
 DQAREKHVKEVISQLTRVHGTSSPYKGLDL-----SKLHETLR  
 GQAREKQVKEAISQLTRGHSTSPYKGLVL-----SKLHETLR  
 RCSFTLHLRSPTTNINETIG---AFQLHITD-----KPSINTDKLK  
 RCSFTLHLRSPTTNINETIG---AFQLHITD-----KPSINTDKLK  
 LCNYTMHISPSTSHENLDLSTHTFKQAMKR-----PDAKWKNPLR  
 -----FSLLDVAPGYDPIWFLNTEP-----SQLP  
 -----MTLLVDAPGYDPLWFITSEP-----TQPP  
 VQLT--IRLKVTSMPAVAVGPDVLAEQRP--SKPLPP--PSREAPP  
 VQFT--IRLKITNMPAVAVGPDVLEQGPRTSLALPPPLPPREAPP  
 IALFSVSRQVSTIMPPQAMGNLVLPEQKPP--SRQSQT----KSKVA  
 FNGTGP-CTNVSTVQCTHGIRPVVSTQLLNLGSLAEVEVIRSVNFTD  
 FSGKKG-CTNVSTVHCTHGIRPVVTTQLLNLGSLAEGNITVRVENKSK  
 YSGFAPNCSKVVASTCTRMETQTSTWFGFNGTRAENRTYIYWHG-RD  
 KLPLSVRVVWRMANLSGWVNGTTPPYWSARINGSTGINGTRWYGVGTLH  
 TVSHVLFCSQDLYGKWYNIENNIQENEQLLTKLYNLTTYSKLRARAL  
 SATLDIYDPKILVSEENVILVSMQYRVASLG-----FLYFDTED  
 -----LQVDADKYKNVNVNGFRVSVREEG-----

gi | 74716 | pir | | VCLJSA  
 gi | 9627213 | ref | NP\_056894.1 |  
 gi | 1706658 | sp | P51515 | ENV\_SRV2  
 gi | 119398 | sp | P10269 | ENV\_BAEVM  
 gi | 1143545 | emb | CAA61093.1 |  
 gi | 9627018 | ref | NP\_041262.1 |  
 gi | 11055586 | gb | AAG28161.1 | AF28  
 gi | 28927670 | gb | AAF81698.2 | AF24  
 gi | 20149612 | ref | NP\_055405.2 |  
 gi | 13310191 | gb | AAK18189.1 | AF33  
 gi | 8439396 | emb | CAB94192.1 |  
 gi | 16024911 | gb | AAL11491.1 |  
 gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO

AHTF-----DLLLATVHSLLNVS-----QRQLAEDCWLCLRSQDP  
 AHTL-----DLLLATVHSLLNAS-----QPSLAEDCWLCLQSGDP  
 AQTF-----NLLTATYSLLNKS-----NPNLANECWLCLPSPGNP  
 AQTL-----NILNATYNLLMS-----NTSLVDDCWLCLKLGPP  
 ARTF-----DILNTTFRLLQMS-----NFSLAQDCWLCLKLGTP  
 AQML-----DILSATHQALNIS-----NPSLAQNCWLCLNQGTS  
 VQTY-----DILASTHKALNIT-----NPD LAKDCWLCLM TLGTP  
 PQTS-----DILEATHQVLNAT-----NPQLAENCWLCLM TLGTP  
 TRLV-----SLFNNTLTGLHEV-----SAQNPTNCWICLPLNFR  
 TRLV-----SLFNNTLTRLHEV-----SAQNPTNCWICLPLHFR  
 SSN-----YCLGRHLPCIS-----LHPWLSPPCSSDSPRPS  
 SSN-----YCLGRHLPCIS-----LHPWLSPPCSSDSPRPS  
 GPPS-----LIFSKPAYYPCTDIKHCHTSPATPMMHCPQAPFG  
 APP-----LLPHSNLDHILE-----PSIPWKSLLTLVQ---  
 SPP-----LVHDSLEHVLV-----PSTSWTTKILKFIQ---  
 LPP-----AASGQAPTVERRTVTLST-----PPPTTGDRFLGLVQGF  
 LPDSNSTALATSQAQPTVRKTIIVTLNT-----PPPTTGDRFLGLVQGF  
 KPQ-----TNGTTPRS-VAPATMSP-----KRIGTRDRLINLVQGTY  
 KTIIVQLDTSVEINCTRPNNNTRKKIRIQRGPGRFVTTIG-KIGNM-R  
 DVWIVQLVEAVSLNCHRPNNNTRGEVQI--GPGMTFYNIENVVGDTR  
 TIIISLNKYNNLSLHCKRPGNKTVKQIML--MSGHVHSHYQPINKRPR

gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHO

GYNISSNPEGGICNFTGELWIGGDRFPYYKPSWNCSQNWGTGHPVWHV  
 EWN-----QGNARLFRSFNPLDVCNRPEAVLLNTTYFTYSLWEGDC  
 GNAG-----LFDQLMALQVWHENIKLFGGNPNNVTLFGESAGA  
 -----LRGLAKGWAPTFIGYSL

gi | 74716 | pir | | VCLJSA  
 gi | 9627213 | ref | NP\_056894.1 |  
 gi | 1706658 | sp | P51515 | ENV\_SRV2  
 gi | 119398 | sp | P10269 | ENV\_BAEVM  
 gi | 1143545 | emb | CAA61093.1 |  
 gi | 9627018 | ref | NP\_041262.1 |  
 gi | 11055586 | gb | AAG28161.1 | AF28  
 gi | 28927670 | gb | AAF81698.2 | AF24  
 gi | 20149612 | ref | NP\_055405.2 |  
 gi | 13310191 | gb | AAK18189.1 | AF33  
 gi | 8439396 | emb | CAB94192.1 |  
 gi | 16024911 | gb | AAL11491.1 |  
 gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO  
 gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHO

LALPYDNTSCSNSTFFFNCSNCSCLITPPFLVQPFNFT-----HSVC  
 LALPYNDTLCSN---FACLSNHSCPLTPPFLVQPFNFT-----DSNC  
 LAIPSNDS-----FLGSNLSCPIIPPLLQPLEFMNL---INASC  
 LAIPNFLLSY---VTRSSDNISCLIIIPPLLQPMQFS-----NSSC  
 LAIPTPSLTYS---LADSLANASCQIIIPPLLQPMQFS-----NSSC  
 LAFPVN-ISS-----FNASQNNCTPSLPFRVQPMPSQ-----VYPC  
 LALLTH-DLS-----FAT---NCALSPFRVQPMRPL-----SAPC  
 AAIPANGNVT-----LDG---NCSLSLPFRVQPTGSI-----DVNC  
 VSIPVPEQWNN-----FSTEINTTSVLVGLVLSNLEIT-----HTSNL  
 ISIPVPEQWNN-----FSTEINTTSVLVGLVLSNLEIT-----HTSNL  
 LLIPSPENNSERLLVDTRRFLIHHENRTFPSTQLPHQS-----PLQP  
 LLIPSPENNSERLLVDTRRFLIHHENRTFPSTQLPHQS-----PLQP  
 YNLTLEFEPDNSTHPVTMSVNPHTFKVKLQGHDRDPYPLS-----HYQP  
 LQSTN-----YTCIVCID-----RAS  
 LQSTN-----YSCMVCVD-----RSS  
 LNATNPGATESCWLCLAMGPPYYEGIASLGEVAYTSDHTR-CRWGTQG  
 LNATNPGATESCWLCLAMGPPYYEAIASSGEVAYSTDLDLDR-CRWGTQG  
 LNATDPNKTKDCWLCLVSRPPYYEGIAILGNYSNQTNPSPSCLSTPQH  
 HCNISRAKWNATLQKIDSKLREQFG-----NNKTIIFKQSS-GGDPEI  
 YCKINGTTWNRTEVEVKALATSSNR---TAANITLNRAS-GGDPEV  
 WCWFKG-KWKDAMQEVKETLAKHPRYRGTNDTRNI SFAAPGKGS DPEV  
 YLDMTEHMTSRCIQRPKRHNI TVGNGTITGNCSVTNWDGCNCTRSGNHI  
 TTALIQLNTECRQPDRLKLPYACRFWRVYKEGQEEVKCLGNEKKKCL'  
 VSLHLLSPLSRNLFNQAIMESGSSTAPWAILSREESFNRG --LKLAKA  
 LCKFG-----

gi | 74716 | pir | | VCLJSA  
 gi | 9627213 | ref | NP\_056894.1 |  
 gi | 1706658 | sp | P51515 | ENV\_SRV2  
 gi | 119398 | sp | P10269 | ENV\_BAEVM  
 gi | 1143545 | emb | CAA61093.1 |  
 gi | 9627018 | ref | NP\_041262.1 |  
 gi | 11055586 | gb | AAG28161.1 | AF28  
 gi | 28927670 | gb | AAF81698.2 | AF24  
 gi | 20149612 | ref | NP\_055405.2 |  
 gi | 13310191 | gb | AAK18189.1 | AF33  
 gi | 8439396 | emb | CAB94192.1 |  
 gi | 16024911 | gb | AAL11491.1 |  
 gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO  
 gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHO

ADYQNNFSDIDVGLAGFTN-----CSSYINIS---  
 AHYQNNFSDIDVGLASFTN-----CSSYINVST--  
 SPFQNNFSDVDVGLVEFAN-----CSTTLNIS--  
 SPSYNSTEEIDLGHVAFSN-----CTSITNVT---  
 SPFINDTEQIDLGAFTFTN-----CTSVANVS---  
 KGAQNNFSDIPVGVANFVN-----CSSSNH----  
 APFRNSSYDLNVGHASFAL-----CTSNHTFN--Y  
 GEADN-RTGIPIGYVHFTN-----CTSIQEVSNET  
 VKFSNTTYTTNSQCIRWVT-----PPT-----  
 VKFSNTIDTSSQCIRWVT-----PPT-----  
 AAALAGSLGVWVQDTPFST-----PSHLFTLH---  
 AAALAGSLGVWVQDAPFST-----PSHLFTLH---  
 GAALSGQYSVWENEITVQENW-----DITSNIFSHLLSFS---  
 TWHVLYSPNVSVPS-SSSTP-----LLYPS----  
 SHVLYTPNISIPQQTSSRT-----ILFPS----  
 TLTEVSGHGLCIGKVPSTHQ-----HLCNQTLPI  
 TLTEVSGHGLCIGKVPFTHQ-----HLCNQTLPI  
 TISEVSGQGLCIGTVPRTHQ-----ALCNKTQQG  
 HSFNCGGEFFYCNSSTQLFNSTWSTKGSNNTEGSDTITLPCRICKIINM  
 HMFNCGGEFFYCNSSTQIFT-----DNITNG--IIILPCRIRQIVSS  
 MWTNCRGEFLYCNMTWFLN-----WIENKTHR---NYAPCHIKQIINT  
 NSTSGLLVVICRQNTITGIMGTNTNWTMWNIIYQNC SRCNNSSLDR  
 SEYSSPEAQFDFGNLSYLNAPFG-----LKYIENQTVREPEYEVYSL  
 CPDDRNTIHKTVCELRKANS-----  
 EVFKVQYNNMLDEETAYTYR-----

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gi | 74716 | pir | | VCLJSA | -----KPSSPLCAPNSSVFVCGNNKAYTYLPTNW-----
gi | 9627213 | ref | NP_056894.1 | -----ASKPSNSLCPNSSVFVCGNNKAYTYLPTNW-----
gi | 1706658 | sp | P51515 | ENV_SRV2 | -----HSLCAPNSSVFVCGNNKAYTYLPSNW-----
gi | 119398 | sp | P10269 | ENV_BAEVM | -----GPICAVNGSVFLCGNNMAYTYLPTNW-----
gi | 1143545 | emb | CAA61093.1 | -----SPLCALNGSVFLCGNNMAYTYLPQNW-----
gi | 9627018 | ref | NP_041262.1 | -----SEALCPGPGQAFVCGNNLAFTALPANW-----
gi | 11055586 | gb | AAG28161.1 | AF28 | -----VERTPHLLCPTPGRAFVCGNNMAFLALPSNW-----
gi | 28927670 | gb | AAF81698.2 | AF24 | -----HIRNLTRLCPPPGHVFCGNNMAYTALPNKW-----
gi | 20149612 | ref | NP_055405.2 | | -----QIVCLPSGIFVFCGTS-AYRCLNGSS-----
gi | 13310191 | gb | AAK18189.1 | AF33 | -----RIVCLPSGIFVFCGTS-AYHCLNGSS-----
gi | 8439396 | emb | CAB94192.1 | | -----LQFCLAQG-LFFLCGSSTYMCLPANW-----
gi | 16024911 | gb | AAL11491.1 | | -----LQFCLAQG-LFFLCGSSTYMCLPANW-----
gi | 27734142 | ref | NP_775596.1 | | -----YAFCLNSSGVFFLCGTSTYICL PANW-----
gi | 119466 | sp | P23064 | ENV_HTL1M | -----LALPAPHLTLPFNWTHCFDPQIQAI-----
gi | 119467 | sp | P03383 | ENV_HTLV2 | -----LALPAP-PSQFPWTHCYQPRLOAI-----
gi | 4027915 | gb | AAC96087.1 | | -----SSKDHQYLLPFNYSWWACSTGLTPCLSTSVFNQ-----
gi | 74689 | pir | | VCLJGL | -----SSGDHQYLLPSNHSWWACSTGLTPCLSTSVFNQ-----
gi | 74707 | pir | | VCMVSS | -----TG--AHYLAAPNGTYWACNTGLTPCISMAVLNW-----
gi | 119431 | sp | P04582 | ENV_HV1B8 | -----QEVGKAMYAPPISGQIRCSSNITGLLLLTRDGGNSNNE-SEI-----
gi | 74661 | pir | | VCLJJSI | -----MRVGRGIYAPPIRGNITCNSNITGLLLLTSDTPVTNNSGNLT-----
gi | 119462 | sp | P04577 | ENV_HV2RO | -----HKVGRNVYLLPPREGELSCNSTVTSIIANIDWQN-NNQTNIT-----
gi | 74682 | pir | | VCLJVS | SGTGLGTVNNLKCSLPHRNESNKWTKSQRDSYIAGRDFWG-----K-----
gi | 74722 | pir | | VCLJLJK | ECMNSAEKYGIDSVLFALKTFLNFTGTPVNEMSTARAFVGLTDPKFPF-----
gi | 12958609 | gb | AAK09373.1 | AF32 | -----SVMVEKEWDHVAICFFPFVPPVVDGAFLDDHP-----
gi | 6016596 | sp | O61703 | MPCP_CHOFO | -----TFVYLAASASAEFFADIALSPLEAAKVR-----

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gi | 74716 | pir | | VCLJSA | -----TGSCVLATLLPDIDIIPGSEPVPIPAIDHFLGRPK-----
gi | 9627213 | ref | NP_056894.1 | | -----TGSCVLATLLPDIDIIPGSEPVPIPAIDHFLGKAK-----
gi | 1706658 | sp | P51515 | ENV_SRV2 | -----TGTCVLATLLPDIDIVPGDAPVVPVPAIDHYLHRAR-----
gi | 119398 | sp | P10269 | ENV_BAEVM | -----TGLCVLATLLPDIDIIPGDEPVPIPAIDHFIYRPK-----
gi | 1143545 | emb | CAA61093.1 | | -----TRLCVQASLLPDIDINPGDEPVPIPAIDHYIHRPK-----
gi | 9627018 | ref | NP_041262.1 | | -----TGSCVLAALLPDIDIISGDDPVPIPTFDYIAGRQK-----
gi | 11055586 | gb | AAG28161.1 | AF28 | -----TGLCVQASILPDINIISGDQPVPLPSIDYIAGRPK-----
gi | 28927670 | gb | AAF81698.2 | AF24 | -----IGLCILASIVPDMSSISGEEPIPLPSIEYTAGRHK-----
gi | 20149612 | ref | NP_055405.2 | | -----ESMCFLSFLVPPMTIYTEQD-----LYNYVISKPRN-----
gi | 13310191 | gb | AAK18189.1 | AF33 | -----ESMCFLSFLVPPMTIYTEQD-----LYNHVVPKPHN-----
gi | 8439396 | emb | CAB94192.1 | | -----TGTCTLVFLTPKIQFANGTEELPVPLMTPTQQ-----
gi | 16024911 | gb | AAL11491.1 | | -----TGTCTLVFLTPKIQFANGTEELPVPLMTPTQQ-----
gi | 27734142 | ref | NP_775596.1 | | -----SGVCTLVFQYPDIELLPNNQTVPVPLFASVLSSDSVLRP-----
gi | 119466 | sp | P23064 | ENV_HTL1M | -----VSSPCHNSLILPPFSLSPVPTLGSRSR-----RAVPV-----
gi | 119467 | sp | P03383 | ENV_HTLV2 | -----TTDNCNNSIILPPFSLAPVPPPATRRR-----RAVPI-----
gi | 4027915 | gb | AAC96087.1 | | -----SRDFCIQIQILPRIYYHPEGTLLQAYDNSHPRLKRE-----
gi | 74689 | pir | | VCLJGL | -----TRDFCIQVQLIPRIYYYPPEVLLQAYDNSHPRTKRE-----
gi | 74707 | pir | | VCMVSS | -----TSDFCVLIELWPRVTYHQPEYIYTHFD-KAVRFRRE-----
gi | 119431 | sp | P04582 | ENV_HV1B8 | PGGGDMRDNRSELYKYKVVKIEPLGVAPTAKARRRVQREK-----
gi | 74661 | pir | | VCLJJSI | PTGGNMKDIWRSELYKYKVVRIEPLSVAPTAKARRHTVARQKDRQK----
gi | 119462 | sp | P04577 | ENV_HV2RO | ---AEVAELYRLELGDYKLVETPIGFAPTKEKRYSSAHGR-----
gi | 74682 | pir | | VCLJVS | AKYSCESNLGGLDSMMHQMLLQRYQVIRVIRAYTYGVVEMPQSYMEER-----
gi | 74722 | pir | | VCLJLJK | PNITKEQKRCNNLKRKRSTNIEKLRSMGYSLTGAVQTLSDINDE-----
gi | 12958609 | gb | AAK09373.1 | AF32 | -----QKSLSTNNFKKTNILMGSNSEEYYSIFYLTELFFK-----
gi | 6016596 | sp | O61703 | MPCP_CHOFO | -----IQTMPGVRQHTARRVAQDGPARGAWARST-----

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gi | 74716 | pir | | VCLJSA | -----RAIQFIPL-VIG-LGITT---AVSTGTAGLGVS---
gi | 9627213 | ref | NP_056894.1 | | -----RAIQLIPL-FVG-LGITT---AVSTGAAGLGVS---
gi | 1706658 | sp | P51515 | ENV_SRV2 | -----RAVQFIPL-LVG-LGITT---AVSTGTAGLGVS---
gi | 119398 | sp | P10269 | ENV_BAEVM | -----RAIQFIPL-LAG-LGITA---AFTTGATGLGVS---
gi | 1143545 | emb | CAA61093.1 | | -----RAVQFIPL-LAG-LGITA---AFTTGATGLGVS---
gi | 9627018 | ref | NP_041262.1 | | -----RAVTLIPL-LVG-LGVST---AVATGTAGLGVA---

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gi | 11055586 | gb | AAG28161.1 | AF28 -----RAVAFIPL-LVG-LGVAG---AMTTGSAGLGVA--
gi | 28927670 | gb | AAF81698.2 | AF24 -----RAVQFIPL-LVG-LGITG---ATLAGGTGLGVS--
gi | 20149612 | ref | NP_055405.2 | -----KRVPIILPF-VIG-AGVLG---ALGTGIGGITTS--
gi | 13310191 | gb | AAK18189.1 | AF33 -----KRVPIILPF-VIR-AGVLG---RLGTGIGSITTS--
gi | 8439396 | emb | CAB94192.1 | -----KRVIPLIPL-MVG-LGLSASTVALGTGIAGISTS--
gi | 16024911 | gb | AAL11491.1 | -----KRVIPLIPL-MVG-LGLSA-----
gi | 27734142 | ref | NP_775596.1 | -----KRSPLFPF-LAG-LGISS---ALGTGIAGLATS--
gi | 119466 | sp | P23064 | ENV_HTL1M -----AVWLVSAL-AMG---AGVAGGI-TGSMSLASG--
gi | 119467 | sp | P03383 | ENV_HTLV2 -----AVWLVSAL-AAG---TGIAGGV-TGSLSLASS--
gi | 4027915 | gb | AAC96087.1 | -----PVSLTLAV-LLG---LGIAAGIGTGSTALIKGPM
gi | 74689 | pir | | VCLJGL -----AVSLTLAV-LLG---LGITAGIGTGSTALIKGPI
gi | 74707 | pir | | VCMVSS -----PISLTVLAV-MLGGLTVGGIAAGVGTGKALLET--
gi | 119431 | sp | P04582 | ENV_HV1B8 -----RAVGIGAL-FLGFLGAAG--STMGAASMTLTVQAR
gi | 74661 | pir | | VCLJSI -----RAAFGLGAL-FLGFLGAAG--STMGAAAVTLTVQAR
gi | 119462 | sp | P04577 | ENV_HV2RO -----HTRGVFVLGFLGFLATAG--SAMGAASLTVSAQSR
gi | 74682 | pir | | VCLJVS NRRSRRNLQRKKGIGLVIVLAIMAIAAAG--AGLGVANAVQQSYTR
gi | 74722 | pir | | VCLJLK -----RLQQGVSLLRDHVVTLMEALHDITIMEGMLAIQHVHT
gi | 12958609 | gb | AAK09373.1 | AF32 -----EENVMVSRENFIKAIQGLNPNADA AVKSAIEFEY--
gi | 6016596 | sp | O61703 | MPCP_CHOF -----

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gi | 74716 | pir | | VCLJSA -----LTQYTKLSHQLISDVQAISSTIQDLQDQVDSLAEVVL
gi | 9627213 | ref | NP_056894.1 | -----ITQYTKLSHQLISDVQAISSTIQDLQDQVDSLAEVVL
gi | 1706658 | sp | P51515 | ENV_SRV2 -----ITQYTKLSRQLISDVQAISSTIQDLQDQVDSLAEVVL
gi | 119398 | sp | P10269 | ENV_BAEVM -----VTQYTKLSNQLISDVQILSSTIQDLQDQVDSLAEVVL
gi | 1143545 | emb | CAA61093.1 | -----VTQYTKLSHQLISDVQVLSGTIQDLQDQVDSLAEVVL
gi | 9627018 | ref | NP_041262.1 | -----VQSYTKLSHQLINDVQALSSTINDLQDQLDSLAEVVL
gi | 11055586 | gb | AAG28161.1 | AF28 -----IHSYAKLSNQLINDVQTLSGTIHDLQDQIDSLAEVVL
gi | 28927670 | gb | AAF81698.2 | AF24 -----VHTYHKLSNQLIEDVQALSSTINDLQDQIDSLAEVVL
gi | 20149612 | ref | NP_055405.2 | -----TQFYKLSQELNGDMERVADSLVTLQDQLNSLAAVVL
gi | 13310191 | gb | AAK18189.1 | AF33 -----TQFYKLSQELNGDMEQVTDLSVTLQDQLNSLAAVVL
gi | 8439396 | emb | CAB94192.1 | -----VMTFRSLSNDFASITDISQTL SVLQAQVDSLAAVVL
gi | 16024911 | gb | AAL11491.1 | -----
gi | 27734142 | ref | NP_775596.1 | -----TLYFQQLSKVLSETLEEIAASITTLQNLQIDSLAGVVL
gi | 119466 | sp | P23064 | ENV_HTL1M -----KSLLEHVDKDISQLTQAI VKNHKNLLKIAQYAA
gi | 119467 | sp | P03383 | ENV_HTLV2 -----KSLLEHVDKDISHLTQAI VKNHQNILRVAQYAA
gi | 4027915 | gb | AAC96087.1 | -----QQGLTSLQIAMADLRAIQDSISKLENSLTSLSEVAL
gi | 74689 | pir | | VCLJGL -----QQGLTSLQIAIDADLRAIQDSISKLENSLTSLSEVVL
gi | 74707 | pir | | VCMVSS -----AQFRQLQIAMHTDIQALEESISALEKSLTSLSEVVL
gi | 119431 | sp | P04582 | ENV_HV1B8 -----LSGIVQQQNNLLRAIEGQQHLLQLTVWGIKQLQARIL
gi | 74661 | pir | | VCLJSI -----LSGIVQQQNNLLKAI EAQQHLLQLSIWGVKQLQARLL
gi | 119462 | sp | P04577 | ENV_HV2RO -----LAGIVQQQQLLDVVKRQQLLRLTVWGTKNLQARVT
gi | 74682 | pir | | VCLJVS -----VQSLANATAAQEVLEASYAMVQHI AKGIRILEARVA
gi | 74722 | pir | | VCLJLK NHLKTILLMRKIDWTFIKSNWIKEQLQKTEDEMKI IRR TAKSLVYYVT
gi | 12958609 | gb | AAK09373.1 | AF32 -----TDWFS PNDPEKNRNALDKMVG DYQFTCNVNEFAHKYA
gi | 6016596 | sp | O61703 | MPCP_CHOF -----RALVPLWGRQIPYTMK FAFKTEVELLYKHVV

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gi | 74716 | pir | | VCLJSA RRGLDLLTAE-----QGGICLA
gi | 9627213 | ref | NP_056894.1 | RRGLDLLTAE-----QGGICLA
gi | 1706658 | sp | P51515 | ENV_SRV2 RRGLDLLTAE-----QGGICLA
gi | 119398 | sp | P10269 | ENV_BAEVM RRGLDLLTAE-----QGGICLA
gi | 1143545 | emb | CAA61093.1 | RRGLDLLTAE-----QGGICLA
gi | 9627018 | ref | NP_041262.1 | RRGLDLLTAE-----QGGICLA
gi | 11055586 | gb | AAG28161.1 | AF28 RRGLDLLTAE-----QGGICLA
gi | 28927670 | gb | AAF81698.2 | AF24 RRGLDLLTAE-----QGGICLA
gi | 20149612 | ref | NP_055405.2 | RRALDLLTAE-----RGGTCLF
gi | 13310191 | gb | AAK18189.1 | AF33 RRALDLLTAK-----RGGTCLF
gi | 8439396 | emb | CAB94192.1 | RRGLDLLTAE-----KGGLCIF
gi | 16024911 | gb | AAL11491.1 | -----

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gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO  
 gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHO

RRALDLITAE-----KGGTCLF  
 RRGLDLLFWE-----QGGLCKA  
 RRGLDLLFWE-----QGGLCKA  
 RRGLDLLFLK-----EGGLCAA  
 RRGLDLLFLK-----EGGLCAA  
 RRGLDILFLQ-----GGGLCAA  
 ERYLKDQQLLGIWGCSGKLICTTAVPWNASWS-NKSLEQIWNMTWME  
 ERYLQDQQILGLWGCSGKAVCYTTVPWNNSWPGSNSTDDIWNLTWQQ  
 EKYLQDQARLNSWGCFAFRQVCHTTVPW-----VNDLAPDWDNMTWQE  
 EALVDMVMVYQELDCWHYQHVCVTSTRSEVAN--YVNWTRFKDNCTWQQ  
 SSSTTATSWEIGIYIEITIPKHIYLNWQVIN----IGHLVESAGHLT  
 GNNVYMYFYK-----HRSLNNP  
 PRAECSKGEQ-----LV

gi | 74716 | pir | | VCLJSA  
 gi | 9627213 | ref | NP\_056894.1 |  
 gi | 1706658 | sp | P51515 | ENV\_SRV2  
 gi | 119398 | sp | P10269 | ENV\_BAEVM  
 gi | 1143545 | emb | CAA61093.1 |  
 gi | 9627018 | ref | NP\_041262.1 |  
 gi | 1105586 | gb | AAG28161.1 | AF28  
 gi | 28927670 | gb | AAF81698.2 | AF24  
 gi | 20149612 | ref | NP\_055405.2 |  
 gi | 13310191 | gb | AAK18189.1 | AF33  
 gi | 8439396 | emb | CAB94192.1 |  
 gi | 16024911 | gb | AAL11491.1 |  
 gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS  
 gi | 119431 | sp | P04582 | ENV\_HV1B8  
 gi | 74661 | pir | | VCLJSI  
 gi | 119462 | sp | P04577 | ENV\_HV2RO  
 gi | 74682 | pir | | VCLJVS  
 gi | 74722 | pir | | VCLJLK  
 gi | 12958609 | gb | AAK09373.1 | AF32  
 gi | 6016596 | sp | O61703 | MPCP\_CHO

EKCCFYA-NKSGIVRDKIKNLQDDLEKRRKQLIDNPFWT-----GFH  
 EKCCFYA-NKSGIVRDKIKNLQDDLEKRRRQLIDNPFWT-----SFH  
 EKCCFYA-NKSGIVRDKIKRLQEDLEKRRKEIIDNPFWT-----GLH  
 EKCCFYV-NKSGIVRDKIKRTLQEELEKRRKDLASNPLWT-----GLQ  
 EKCCFYA-NKSGIVRDKIKRTLQEELEKRRKDLASNPLWT-----GLQ  
 ERCCFYA-NKSGIVRDKIKNLQEDLEKRRKALADNLFILT-----GLN  
 EKCCFYA-NKSGMVRDKIKKLQEEELVQRRKELLNPLWN-----GLH  
 EKCCFYA-NKSGIVRDKIKRLQEDLIARKRALYDNPLWN-----GLN  
 EECCYYV-NQSGIVTEKVKIIRDRIQRRAEELRNTGPWG-----LLS  
 EERCYYV-NQSRIVTEKVKIIRDRIQCRAEELQNTERWG-----LLS  
 EECCFYL-NQSGLVYDNIKKLDRAQKLANQASNYAEPW-----ALS  
 -----  
 EECCFYV-NQSGIVRDAARKLQERASELGQHSWSWGWQP-----DLG  
 EQCCFLN-ITN----SHVSILQERP---PLENRVLTGWGLNWDLGLSQ  
 EQCCFLN-ISN----THVSVLQERP---PLEKRVITGWGLNWDLGLSQ  
 EECCFYV-DHSGAVRDSMRKLERLDRKQLERQKNQNWYEGWFN-SSP  
 EECCFYI-DHSGAVRDSMKKLEKLDKRLERQKSQNWYEGWFN-NSP  
 EECCFYA-DHTGLVRDNMAKLRERLKRQQLFDSQQGWFEWGFN-KSP  
 REINNYT-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWFDITKWL  
 KLVSNYT-GKIFGLLEEAQSQQEKNERDLLELDQWASLWNWFDITKWL  
 KQVRYLE-ANISKSLEQAQIQQEKMYELQKLNWDIFGNWFDLTSWV  
 EEIEQHEGNLSLLLEAALQVHIAQRDARRIPDAWKAIQEAFNSSWF  
 RVKHPEYEVINKECTYEQYLHLEDCISQDYVICDTVQIVSPCGNSTTTSI  
 KWTGVMHGDEISYVFGDPLNPNKRYEIEEIELSKMMRYWTNFAKTGNI  
 FAAGYIAGVFCIAIVSHPADTVVSKLNQDKTATVGS-----IVGKL

gi | 74716 | pir | | VCLJSA  
 gi | 9627213 | ref | NP\_056894.1 |  
 gi | 1706658 | sp | P51515 | ENV\_SRV2  
 gi | 119398 | sp | P10269 | ENV\_BAEVM  
 gi | 1143545 | emb | CAA61093.1 |  
 gi | 9627018 | ref | NP\_041262.1 |  
 gi | 1105586 | gb | AAG28161.1 | AF28  
 gi | 28927670 | gb | AAF81698.2 | AF24  
 gi | 20149612 | ref | NP\_055405.2 |  
 gi | 13310191 | gb | AAK18189.1 | AF33  
 gi | 8439396 | emb | CAB94192.1 |  
 gi | 16024911 | gb | AAL11491.1 |  
 gi | 27734142 | ref | NP\_775596.1 |  
 gi | 119466 | sp | P23064 | ENV\_HTL1M  
 gi | 119467 | sp | P03383 | ENV\_HTLV2  
 gi | 4027915 | gb | AAC96087.1 |  
 gi | 74689 | pir | | VCLJGL  
 gi | 74707 | pir | | VCMVSS

LPYVMPPLGPLLCLLLVLSFGPIIFNKLMTFIKHQ-----IESIQ  
 LPYVMPPLGPLLCLLLVLSFGPIIFNKLMTFIKHQ-----IESIQ  
 LPYLLPLLGPLFCLLLLITFGPLIFNKIITFVKQQ-----IDAIQ  
 LPYLLPFLGPLLTLTLLLTIGPCIFNRLTAFINDK-----LNIIH  
 LPYLLPLLGPLLTLTLLILTIGPCVFSRLMAFINDR-----LNVVH  
 LPYLLPFLGPLFAIILFFSFAPWILRRVTALIRDQ-----LNSLL  
 LPYLLPLLGPLVGLLLLLSFGPWVFNRLTTFVKSQ-----VDSAI  
 LPYLLPLLGPLFGLIFLTLGPCIIKTLTRI IHDK-----IQAVK  
 MPWILPFLGPLAAIILLLLFGPCIFNLLVNFVSSR-----IEAVK  
 MPWTL PFLGPLAAIIFLLLFGPCIFNFLVKFVSSR-----IEAVK  
 MSWVLPVSPILPIIFLLLFGPCIFRLVSQFIQNR-----IQAIT  
 -----  
 LPWLTPFLGPLLFLFLLTTFGSCLLNCLTRFVSQR-----LGSFV  
 REALQTGITLVALLLLVLVLAGPCILRQLRHLPSRV-----RYPH-  
 REALQTGITILALLLLLVLVLAGPCILRQIQALPQRL-----QNRHN  
 TTLLSTIAGPLLLLLLLLILGPCIINRLVQFINDR-----VSAVK  
 TTLLSTIAGPLLLLLLLLILGPCIINKLVQFINDR-----ISAC-  
 TTLISSIMGPLLILLLLLILVLAGPCILNRLVQFVKDR-----ISVVQ





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